Claim 8 (currently amended): The method of claim 1, wherein said polymorphic site is in a TNF-α regulatory region that regulates expression of TNF-α.

Claim 9 (original): The method of claim 8, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

Claim 10 (original): The method of claim 9, wherein said polymorphic site is in a TNF-α promoter region.

Claim 11 (original): The method of claim 1, wherein said polymorphic site is in a TNF-α coding region.

Claim 12 (original): The method of claim 1, wherein said liver transplant donor is identified for transplantation into a hepatitis C virus infected patient.

Claim 13 (currently amended): A method for selecting a preferred liver for transplantation, comprising the steps of:

(a) ~~obtaining material from one or more potential liver donors~~;

(a) ~~(b)~~ determining in said one or more potential liver donors the presence or absence of a preferred genotype at a polymorphic site, said preferred genotype associated with altered activity of [a] tumor necrosis factor-α (TNF-α), and wherein said polymorphic site is in a genomic nucleic acid sequence encoding interleukin (IL)-1, IL-2, IL-6, IL-8, transforming growth factor (TGF)-β, IL-10, granulocyte macrophage colony stimulating factor (GMCSF), ciliary neurotrophic factor (CNTF) or TNF-α; and

(b) ~~(c)~~ harvesting a liver, or functional portion thereof, having a preferred genotype; thereby selecting a preferred liver for transplantation.

Claim 14 (currently amended): The method of claim 13, further comprising the step of:

(c) ~~(d)~~ transplanting said liver, or functional portion thereof, into a recipient.

Claim 8 (currently amended): The method of claim 1, wherein said polymorphic site is in a TNF-α regulatory region that regulates expression of TNF-α.

Claim 9 (original): The method of claim 8, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

Claim 10 (original): The method of claim 9, wherein said polymorphic site is in a TNF-α promoter region.

Claim 11 (original): The method of claim 1, wherein said polymorphic site is in a TNF-α coding region.

Claim 12 (original): The method of claim 1, wherein said liver transplant donor is identified for transplantation into a hepatitis C virus infected patient.

Claim 13 (currently amended): A method for selecting a preferred liver for transplantation, comprising the steps of:

(a) ~~obtaining material from one or more potential liver donors~~;

(a) ~~(b)~~ determining in said one or more potential liver donors the presence or absence of a preferred genotype at a polymorphic site, said preferred genotype associated with altered activity of [a] tumor necrosis factor-α (TNF-α), and wherein said polymorphic site is in a genomic nucleic acid sequence encoding interleukin (IL)-1, IL-2, IL-6, IL-8, transforming growth factor (TGF)-β, IL-10, granulocyte macrophage colony stimulating factor (GMCSF), ciliary neurotrophic factor (CNTF) or TNF-α; and

(b) ~~(c)~~ harvesting a liver, or functional portion thereof, having a preferred genotype; thereby selecting a preferred liver for transplantation.

Claim 14 (currently amended): The method of claim 13, further comprising the step of:

(c) ~~(d)~~ transplanting said liver, or functional portion thereof, into a recipient.

Claim 15 (currently amended): The method of claim 13, wherein said preferred genotype is associated with lower activity of ~~said~~ tumor necrosis factor-α.

Claim 16 (canceled).

Claim 17 (currently amended): The method of claim 15, wherein said preferred genotype is associated with lower levels of ~~said~~ tumor necrosis factor-α.

Claim 18 (canceled).

Claim 19 (currently amended): The method of claim [18] 17, wherein said preferred genotype is TNF308.1.

Claim 20 (original): The method of claim 13, wherein said polymorphic site is in a TNF-α regulatory region.

Claim 21 (original): The method of claim 20, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

Claim 22 (original): The method of claim 21, wherein said polymorphic site is in a TNF-α promoter region.

Claim 23 (original): The method of claim 13, wherein said polymorphic site is in a TNF-α coding region.

Claim 24 (original): The method of claim 14, wherein said recipient is infected with hepatitis C virus.

Claim 25-34 (canceled).

Claim 35 (new): The method of claim 1, wherein said preferred genotype is a guanine (G) at position -380 in a gene encoding TNF-α.

Claim 36 (new): The method of claim 13, wherein said preferred genotype is a guanine (G) at position -380 in a gene encoding TNF-α.

Claim 37 (new): A method of identifying a preferred liver transplant donor, comprising

determining in an individual a presence or an absence of a preferred genotype at a polymorphic site, wherein said preferred genotype comprises a guanine (G) at position -380 in a tumor necrosis factor (TNF) α promoter,

wherein the presence of said preferred genotype indicates that said individual is a preferred liver transplant donor.

Claim 38 (new): A method for selecting a preferred liver for transplantation, comprising

determining in one or more potential liver donors the presence or absence of a preferred genotype at a polymorphic site, wherein said preferred genotype comprises a guanine (G) at position -380 in a tumor necrosis factor (TNF) α promoter; and

harvesting a liver, or functional portion thereof, having said preferred genotype;

thereby selecting said preferred liver for transplantation.

Claims 39 (new): The method of claim 13, further comprising the step of:

(c) transplanting said liver, or functional portion thereof, into a recipient.

Claim 40 (new): The method of claim 39, wherein said recipient is infected with hepatitis C virus.